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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/722,441

DATE: 07/05/2001  
TIME: 16:42:45

#3

Input Set : A:\1533 1030002 seq list.txt  
Output Set: N:\CRF3\07032001\I722441.raw

5 <110> APPLICANT: Hanke, Paul D.  
7 Li-D'Elia, Lhing-Yew  
9 Rayapati, John  
11 Crafton, Corey  
13 Walsh, Holly  
17 <120> TITLE OF INVENTION: Increased Lysine Production by Gene Amplification  
21 <130> FILE REFERENCE: 1533.1030002  
25 <140> CURRENT APPLICATION NUMBER: 09/722,441  
C--> 27 <141> CURRENT FILING DATE: 2001-06-22  
30 <150> PRIOR APPLICATION NUMBER: US 60/173,707  
31 <151> PRIOR FILING DATE: 1999-12-30  
34 <150> PRIOR APPLICATION NUMBER: US 60/184,130  
35 <151> PRIOR FILING DATE: 2000-02-22  
39 <160> NUMBER OF SEQ ID NOS: 37  
43 <170> SOFTWARE: PatentIn version 3.0  
47 <210> SEQ ID NO: 1  
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51 <212> TYPE: DNA  
53 <213> ORGANISM: Corynebacterium glutamicum  
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59 <221> NAME/KEY: CDS  
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68 1 5 10 15  
70 gaa cgc att aga aac gtc gct gaa cg<sup>g</sup> atc gtt gcc acc aag aag gct 96  
71 Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala  
72 20 25 30  
74 gga aat gat gtc gtg gtc tgc tcc gca atg gga gac acc acg gat 144  
75 Gly Asn Asp Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp  
76 35 40 45  
78 gaa ctt cta gaa ctt gca gca gtg aat ccc gtt ccg cca gct cgt 192  
79 Glu Leu Leu Glu Leu Ala Ala Val Asn Pro Val Pro Pro Ala Arg  
80 50 55 60  
82 gaa atg gat atg ctc ctg act gct ggt gag cgt att tct aac gct ctc 240  
83 Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu  
84 65 70 75 80  
86 gtc gcc atg gct att gag tcc ctt ggc gca gaa gct caa tct ttc act 288  
87 Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr  
88 85 90 95  
90 ggc tct cag gct ggt gtg ctc acc acc gag cgc cac gga aac gca cgc 336  
91 Gly Ser Gln Ala Gly Val Leu Thr Glu Arg His Gly Asn Ala Arg  
92 100 105 110  
94 att gtt gac gtc aca ccg ggt gtg cgt gaa gca ctc gat gag ggc 384  
95 Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly  
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Input Set : A:\1533 1030002 seq list.txt  
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100 130 135 140	
102 gat gtc acc acg ttg ggt cgt ggt ggt tct gac acc act gca gtt gcg	480
103 Asp Val Thr Thr Leu Gly Arg Gly Ser Asp Thr Thr Ala Val Ala	
104 145 150 155 160	
106 ttg gca gct gct ttg aac gct gat gtg tgt gag att tac tcg gac gtt	528
107 Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val	
108 165 170 175	
110 gac ggt gtg tat acc gct gac ccg cgc atc gtt cct aat gca caq aag	576
111 Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys	
112 180 185 190	
114 ctg gaa aag ctc agc ttc gaa gaa atg ctg gaa ctt gct gct gtt ggc	624
115 Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly	
116 195 200 205	
118 tcc aag att ttg gtg ctg cgc agt gtt gaa tac gct cgt gca ttc aat	672
119 Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn	
120 210 215 220	
122 gtg cca ctt cgc gta cgc tcg tct tat agt aat gat ccc ggc act ttg	720
123 Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu	
124 225 230 235 240	
126 att gcc ggc tct atg gag gat att cct gtg gaa gaa gca gtc ctt acc	768
127 Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr	
128 245 250 255	
130 ggt gtc gca acc gac aag tcc gaa gcc aaa gta acc gtt ctg ggt att	816
131 Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile	
132 260 265 270	
134 tcc gat aag cca ggc gag gct gcc aag gtt ttc cgt gcg ttg gct gat	864
135 Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp	
136 275 280 285	
138 gca gaa atc aac att gac atg gtt ctg cag aac gtc tcc tct gtg gaa	912
139 Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu	
140 290 295 300	
142 gac ggc acc acc gac atc acg ttc acc tgc cct cgc gct gac gga cgc	960
143 Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ala Asp Gly Arg	
144 305 310 315 320	
146 cgt gcg atg gag atc ttg aag aag ctt cag gtt cag ggc aac tgg acc	1008
147 Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr	
148 325 330 335	
150 aat gtg ctt tac gac gac cag gtc ggc aaa gtc tcc ctc gtg ggt gct	1056
151 Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala	
152 340 345 350	
154 ggc atg aag tct cac cca ggt gtt acc gca gag ttc atg gaa gct ctg	1104
155 Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu	
156 355 360 365	
158 cgc gat gtc aac gtg aac atc gaa ttg att tcc atc tct gag atc cgc	1152
159 Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Ile Ser Glu Ile Arg	
160 370 375 380	
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164 385 390 395 400
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171 Ala Gly Thr Gly Arg
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179 <212> TYPE: PRT
181 <213> ORGANISM: Corynebacterium glutamicum
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188 1 5 10 15
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195 Gly Asn Asp Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
196 35 40 45
199 Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg
200 50 55 60
203 Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
204 65 70 75 80
207 Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
208 85 90 95
211 Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
212 100 105 110
215 Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
216 115 120 125
219 Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
220 130 135 140
223 Asp Val Thr Thr Leu Gly Arg Gly Ser Asp Thr Thr Ala Val Ala
224 145 150 155 160
227 Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
228 165 170 175
231 Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
232 180 185 190
235 Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
236 195 200 205
239 Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
240 210 215 220
243 Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu
244 225 230 235 240
247 Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr
248 245 250 255
251 Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile
252 260 265 270
255 Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp
256 275 280 285

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Input Set : A:\1533 1030002 seq list.txt  
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259 Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu  
 260 290 295 300  
 263 Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ala Asp Gly Arg  
 264 305 310 315 320  
 267 Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr  
 268 325 330 335  
 271 Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala  
 272 340 345 350  
 275 Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu  
 276 355 360 365  
 279 Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Ile Ser Glu Ile Arg  
 280 370 375 380  
 283 Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala  
 284 385 390 395 400  
 287 Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr  
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 292 420  
 295 <210> SEQ ID NO: 3  
 297 <211> LENGTH: 1035  
 299 <212> TYPE: DNA  
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 305 <220> FEATURE:  
 307 <221> NAME/KEY: CDS  
 309 <222> LOCATION: (1)..(1035)  
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 316 1 5 10 15  
 318 atg cgc acc ttt ttg gaa gag cgc aat ttc cca gct gac act gtt cgt 96  
 319 Met Arg Thr Phe Leu Glu Glu Arg Asn Phe Pro Ala Asp Thr Val Arg  
 320 20 25 30  
 322 ttc ttt gct tcc ccg cgt tcc gca ggc cgt aag att gaa ttc cgt ggc 144  
 323 Phe Phe Ala Ser Pro Arg Ser Ala Gly Arg Lys Ile Glu Phe Arg Gly  
 324 35 40 45  
 326 acg gaa atc gag gta gaa gac att act cag gca acc gag gag tcc ctc 192  
 327 Thr Glu Ile Glu Val Glu Asp Ile Thr Gln Ala Thr Glu Glu Ser Leu  
 328 50 55 60  
 330 aag ggc atc gac gtt gcg ttg ttc tct gct gga ggc acc gct tcc aag 240  
 331 Lys Gly Ile Asp Val Ala Leu Phe Ser Ala Gly Gly Thr Ala Ser Lys  
 332 65 70 75 80  
 334 cag tac gct cca ctg ttt gct gct gca ggc gcg act gtt gtg gat aac 288  
 335 Gln Tyr Ala Pro Leu Phe Ala Ala Gly Ala Thr Val Val Asp Asn  
 336 85 90 95  
 338 tct tct gct tgg cgc aag gac gac gag gtt cca cta atc gtc tct gag 336  
 339 Ser Ser Ala Trp Arg Lys Asp Asp Glu Val Pro Leu Ile Val Ser Glu  
 340 100 105 110  
 342 gtg aac cct tcc gac aag gat tcc ctg gtc aag ggc att att gcg aat 384  
 343 Val Asn Pro Ser Asp Lys Asp Ser Leu Val Lys Gly Ile Ile Ala Asn

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344	115	120	125	
346	cct aac tgc acc acc atg gct gca atg cca gtg ctg aag cca ctg cac			432
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348	130	135	140	
350	gat gcc gct ggt ctt gta aag ctt cac gtt tcc tct tac cag gct gtt			480
351	Asp Ala Ala Gly Leu Val Lys Leu His Val Ser Ser Tyr Gln Ala Val			
352	145	150	155	160
354	tcc ggt tct ggt ctt gca ggt gtg gaa acc ttg gca aag cag gtt gct			528
355	Ser Gly Ser Gly Leu Ala Gly Val Glu Thr Leu Ala Lys Gln Val Ala			
356	165	170	175	
358	gca gtt ggc gac cac aac gtt gag ttc gtc cat gat gga cag gct gct			576
359	Ala Val Gly Asp His Asn Val Glu Phe Val His Asp Gly Gln Ala Ala			
360	180	185	190	
362	gac gca ggc gat gtc gga cct tac gtt tcc cca atc gct tac aac gtg			624
363	Asp Ala Gly Asp Val Gly Pro Tyr Val Ser Pro Ile Ala Tyr Asn Val			
364	195	200	205	
366	ctg cca ttc gcc gga aac ctc gtc gat gac ggc acc ttc gaa acc acc gac			672
367	Leu Pro Phe Ala Gly Asn Leu Val Asp Asp Gly Thr Phe Glu Thr Asp			
368	210	215	220	
370	gaa gag cag aag ctg cgc aac gaa tcc cgc aag att ctc ggc ctc cca			720
371	Glu Glu Gln Lys Leu Arg Asn Glu Ser Arg Lys Ile Leu Gly Leu Pro			
372	225	230	235	240
374	gac ctc aag gtc tca ggc acc tgc gtc cgc gtg ccg gtt ttc acc ggc			768
375	Asp Leu Lys Val Ser Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly			
376	245	250	255	
378	cac acg ctg acc att cac gcc gaa ttc gac aag gca atc acc gtc gag			816
379	His Thr Leu Thr Ile His Ala Glu Phe Asp Lys Ala Ile Thr Val Glu			
380	260	265	270	
382	cag gcg cag gag atc ttg ggt gcc gct tca ggc gtc gag ctt gtc gac			864
383	Gln Ala Gln Glu Ile Leu Gly Ala Ala Ser Gly Val Glu Leu Val Asp			
384	275	280	285	
386	gtc cca acc cca ctt gca gct gcc ggc att gac gaa tcc ctc gtt gga			912
387	Val Pro Thr Pro Leu Ala Ala Gly Ile Asp Glu Ser Leu Val Gly			
388	290	295	300	
390	cgc atc cgt cag gac tcc act gtc gac gac aac cgc ggt ctg gtt ctc			960
391	Arg Ile Arg Gln Asp Ser Thr Val Asp Asp Asn Arg Gly Leu Val Leu			
392	305	310	315	320
394	gtc gta tct ggc gat aac ctt cgc aag ggc gca gca ctg aac acc att			1008
395	Val Val Ser Gly Asp Asn Leu Arg Lys Gly Ala Ala Leu Asn Thr Ile			
396	325	330	335	
398	cag att gct gag ctg ctg gtt aag taa			1035
399	Gln Ile Ala Glu Leu Leu Val Lys			
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405	<211> LENGTH: 344			
407	<212> TYPE: PRT			
409	<213> ORGANISM: Corynebacterium glutamicum			
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**VERIFICATION SUMMARY**

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Output Set: N:\CRF3\07032001\I722441.raw

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L:2091 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:25  
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L:2235 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:33  
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